

Figure 1

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1  ACCCTTCCTGGGCCCCAGTCTACCCGGCTTGAAGGTGCCCGCCCTCCTTTGGAGAGTGTCCTC
61  GGAGCAGACAGTATGGAGGGGAGCCCTCCCAGCCCTCCCAACGGCAGCTGGCCCCCTGGGT
121  CAGAACGGGAGTGATGTGGAGACCAGCATGGCAACACAGCCTCACCTTCTCCTACTACTAC
181  CAACACTCCTCTCCGGTGGCAGCCATGTTTCATCGGGCCCTACGTGCTCATCTTCTCCTCCTC
241  TGCATGGTGGGCAACACCCTGGTCTGCTTTCATTTGCTCAAGAACCGGCACATGCGCACT
301  GTCACCAACATGTTTATCCTCAACCTGGCCGTCAGCGACCTGCTGGTGGGCATCTTCTGTC
361  ATGCCCCAACCCCTTGTGGACAACCTTATCACTGGTTGGCCTTTTGACAAAGCCACATGC
421  AAGATGAGCGGCTTGGTGCAAGGCATGTCGGTGCTGTCATCGGTTTTCACACTGCTGGGCC
481  ATCGCTGTGGAAGGTTCCGCTGCATCGTGACCCCTTTCCGGGAGAAAGCTGACCCCTTCGG
541  AAGCGCTGTTCAACCATCGCGGTGATCTGGGCTCTGGCGCTGCTCATCATGTGTCCCTCG
601  GCGGTCACTCTGACAGTACCCGAGAGGAGCATCACTTCATGCTGGATGCTCGTAACCGC
661  TCCTACCCGCTCTACTCTCGGACATCTACCTGGTGCCGCTGGCCGAGAAAGGCATGCCAAGTCTAC
721  ACCGCGGTGCTCTTCGGGACATCTACCTGGTGCCGCTCCGTCCTGCGGGACACGGAGGAGCG
781  GTGCGCATCGCGCAAGCTATGCCAGGCCCCCGTCCGTGCTGCGGACACATGCTGGTCAATG
841  GTGGCCGAGGGTGGCCGCACTTCGCGCCGTAGGGCCCGCTGGTGCTGCTGCTCATCGAC
901  GTGGCGCTCTTCTTACGTTGTCTGGCTGCCACTCTGGGTGCTGCTGCTGCTGCTGCTGCTG
961  TATGGGGAGCTGAGCGAGCTGCAACTGCACCTGCTGTCGGTCTACGCCCTTCCCTTGGCA
1021  CACTGGCTGGCCTTCTTCCACAGCAGCGCAACCCCATCATCTACGGCTACTTCAACGAG
1081  AACTTCGCGCGGGCTTCCAGGCTGCCCTCCGTGCACAGCTCTGCTGGCCCTCCCTGGGCC
1141  GCCCAAGCAAGCCTACTCGGAGCGGGCCCAACCGCCTCCTGGCAGCGGGTGGTGGTG
1201  GACGTGCAACCCAGCGACTCCGGCCTGCCATCAGAGTCTGGCCCCAGCAGCGGGGTCCCA
1261  GGGCCTGGCCGGCTGCCACTGCGCAATGGGCGTGTGGCCCATCAGGATGGCCCGGGGAA
1321  GGGCCAGGCTGCAACCCACATGCCCTTACCATCCCGGCTGGAAACATTTGAGGTGGTCCA
1381  GAGAGGGAGGGCCAGTAGTCCTGTGGCCC
1410

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Figure 2

1 M E A E P S Q P P N G S W P L G Q N G S 20  
21 D V E T S M A T S L T F S S Y Y Q H S S 40  
41 P V A A M F I A A Y V L I F L L C M V G 60  
61 N T L V C F I V L K N R H M R T V T N M 80  
81 F I L N L A V S D L L V G I F C M P T T 100  
101 L V D N L I T G W P F D N A T C K M S G 120  
121 L V Q G M S V S A S V F T L V A I A V E 140  
141 R F R C I V H P F R E K L T L R K A L F 160  
161 T I A V I W A L A L L I M C P S A V T L 180  
181 T V T R E E H H F M L D A R N R S Y P L 200  
201 Y S C W E A W P E K G M R K V Y T A V L 220  
221 F A H I Y L V P L A L I V V M Y V R I A 240  
241 R K L C Q A P G P A R D T E E A V A E G 260  
261 G R T S R R R A R V V H M L V M V A L F 280  
281 F T L S W L P L W V L L L L I D Y G E L 300  
301 S E L Q L H L L S V Y A F P L A H W L A 320  
321 F F H S S A N P I I Y G Y F N E N F R R 340  
341 G F Q A A F R A Q L C W P P W A A H K Q 360  
361 A Y S E R P N R L L R R R V V V D V Q P 380  
381 S D S G L P S E S G P S S G V P G P G R 400  
401 L P L R N G R V A H Q D G P G E G P G C 420  
421 N H M P L T I P A W N I 432

- Figure 3 -

1 M E A E P S Q P P N G S W P L G Q N G S 20  
 21 D V E T S M A T S L T F S S Y Y Q H S S 40  
 41 P V A A M F I A A Y V L I F L L C M V G 60  
 61 N T L V C F I V L K N R H M R T V T N M 80  
 81 F I L N L A V S D L L V G I F C M P T T 100  
 101 L V D N L I T G W P F D N A T C K M S G 120  
 121 L V O G M S V S A S V F T L V A I A V E 140  
 141 R F R C I V H P F R E K L T L R K A L F 160  
 161 T I A V I W A L A L L I M C P S A V T L 180  
 181 T V T R E E H H F M L D A R N R S Y P L 200  
 201 Y S C W E A W P E K G M R K V Y T A V L 220  
 221 F A H I Y L V P L A L I V V M Y V R I A 240  
 241 R K L C Q A P G P A R D T E E A V A E G 260  
 261 G R T S R R R A R V V H M L V M V A L F 280  
 281 F T L S W L P L W V L L L L I D Y G E L 300  
 301 S E L Q L H L L S V Y A F P L A H W L A 320  
 321 F F H S S A N P I I Y G Y F N E N F R R 340  
 341 G F Q A A F R A Q L C W P P W A A H K Q 360  
 361 A Y S E R P N R L L R R R V V V D V Q P 380  
 381 S D S G L P S E S G P S S G V P G P G R 400  
 401 L P L R N G R V A H Q D G P G E G P G C 420  
 421 N H M P L T I P A W N I 432

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Figure 4

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1  GAGCCCTCCCAGCCTCCCAACAGCAGTTGGCCCCCTAAGTCAGAATGGGACTAACA CTGAG 60
61  GCCACCCCGGCTACAAACCTCACCTTCTCCTCCTACTATCAGCACACCTCCCCCTGTGGCG 120
121  GCCATGTTTCATTGTGGCCTATGGGCTCATCTTCCTGCTCTGCATGGTGGGCAACACCCCTG 180
181  GTCTGTTTCATCGTGTCTCAA 200
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Figure 6

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1 MEAEPSQPPNGSWPLQNGSDVETSMATSLTFSSYYQHSSPVAAMFIAAY rNPFF1
  ||||| ||| |||.. | . ||.|||||||.|||||| ||
1 ...EPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAY hNPFF1

51 VLIFLLCMVGNTLVCFIVL rNPFF1
  ||||| ||| ||| ||| |||
48 ALIFLLCMVGNTLVCFIVL hNPFF1
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Figure 7

1 GCCACAGGGCTCGCCGGGAGAGGTTTCATCATGAATGAGAAAATGGGACACAAACTCTTCA 60  
 61 GAAAACTGGCATCCCATCTGGAATGTCAATGACACAAAGCATCATCTGTACTCAGATATT 120  
 121 AATATTACCTATGTGAACACTACTATCTTACCAGCCTCAAGTGGCAGCAATCTTCATTATT 180  
 181 TCCTACTTTCTGATCTTCTTTTGTGTCATGATGGGAAATACTGTGGTTTGCTTTATTGTA 240  
 241 ATGAGGAACAAACATATGCACACAGTCACATAATCTCTTCATCTTAAACCTGGCCATAAGT 300  
 301 GATTACTAGTTGGCATATTCTGCATGCCATAACACTGCTGGACAAATATATAGCAGGA 360  
 361 TGGCCATTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCAGGGAATATCTGTGCA 420  
 421 GCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCAGTGTGGTCTACCCCT 480  
 481 TTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCAATTATTATGATCATCTGGGTCTTA 540  
 541 GCCATCACCATTATGTCCTCCATCTGCAGTAATGTTACATGTGCAAGAAGAAAATATTAC 600  
 601 CGAGTGAGACTCAACTCCAGAAATAAAACCACTCAGTCCAGTCTACTGGTCCCGGGAAGACTGG 660  
 661 CCAAATCAGGAAATGAGGAAGATCTACACCACCTGTGCTGTTTGCCAAACATCTACCTGGCT 720  
 721 CCCCTCTCCCTCATTTGTCATCATGTATGGAAGGATTGGAATTTCACTCTTCAGGGCTGCA 780  
 781 GTTCCTCACACAGGCAGGAAGAACCCAGGAGCAGTGGCACGTGGTGTCAGGAAGAAGCAG 840  
 841 AAGATCATTAAGATGCTCCTGATTGTGGCCCTGCTTTTATTCTCTCATGGTCCCCCTG 900  
 901 TGGACTCTAATGATGCTCTCAGACTACGCTGACCTTCTCCAAATGAACATGCAGATCATC 960  
 961 AACATCTACATCTACCCCTTTTGACACACTGGCTGGCATTCGGCAACACAGCAGTGTCAATCCC 1020  
 1021 ATCATTTATGGTTTCTTCAACGAGAAATTTCCGCCGTGGTTTCCAAGAAGCTTCCAGCTC 1080  
 1081 CAGCTCTGCCAAAAAAGAGCAAGCCCTATGGAAGCTTATGCCCTAAAAGCTAAAAGCCAT 1140  
 1141 GTGCTCATAAACACATCTAATCAGCTTGTCCAGGAATCTACATTTCAAAACCCCTCATGGG 1200  
 1201 GAAACCTTGCTTTATAGGAAAAGTGCTGAAAAACCCCAACAGGAATTAGTGATGGAAGAA 1260  
 1261 TTAAAGAAACTACTAACAGCAGTGAGATTTAAAAAGAGCTA 1302

- Figure 8

[illegible]



Variable	Mean	SD	Min	Max	Median	Q1	Q3	Mode	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.2	12.5	22	65	33	28	38	33	0.15	2.10	0.98	Normal
Gender	1.2	0.4	1	2	1	1	1	1	0.05	0.10	0.99	Normal
Marital Status	2.1	0.8	1	3	2	1	3	2	0.10	0.50	0.99	Normal
Education	15.8	2.5	10	20	16	15	17	16	0.08	0.30	0.99	Normal
Income	1200	300	500	2500	1100	800	1400	1100	0.12	0.80	0.98	Normal
Occupation	1.5	0.5	1	3	1	1	2	1	0.05	0.10	0.99	Normal
Health Status	2.5	0.5	1	3	2	2	2	2	0.02	0.05	0.99	Normal
Stress Level	3.2	1.0	1	5	3	2	4	3	0.18	2.50	0.97	Normal
Life Satisfaction	4.1	0.8	3	5	4	4	4	4	0.03	0.10	0.99	Normal
Work-Life Balance	3.8	0.9	2	5	4	3	4	4	0.04	0.20	0.99	Normal
Family Support	4.5	0.6	3	5	4	4	4	4	0.01	0.05	0.99	Normal
Community Involvement	2.8	0.7	1	4	3	2	3	3	0.06	0.40	0.99	Normal
Volunteering	1.8	0.6	1	3	2	1	2	2	0.04	0.20	0.99	Normal
Charitable Giving	1.5	0.5	1	3	1	1	2	1	0.05	0.10	0.99	Normal
Political Participation	1.2	0.4	1	2	1	1	1	1	0.03	0.10	0.99	Normal
Environmental Awareness	3.5	0.8	2	5	3	3	3	3	0.02	0.10	0.99	Normal
Social Media Usage	2.2	0.7	1	4	2	1	3	2	0.07	0.30	0.99	Normal
Digital Literacy	3.0	0.9	1	5	3	2	4	3	0.06	0.40	0.99	Normal
Online Learning	2.5	0.8	1	4	2	1	3	2	0.08	0.50	0.98	Normal
Work-Life Balance	3.8	0.9	2	5	4	3	4	4	0.04	0.20	0.99	Normal
Family Support	4.5	0.6	3	5	4	4	4	4	0.01	0.05	0.99	Normal
Community Involvement	2.8	0.7	1	4	3	2	3	3	0.06	0.40	0.99	Normal
Volunteering	1.8	0.6	1	3	2	1	2	2	0.04	0.20	0.99	Normal
Charitable Giving	1.5	0.5	1	3	1	1	2	1	0.05	0.10	0.99	Normal
Political Participation	1.2	0.4	1	2	1	1	1	1	0.03	0.10	0.99	Normal
Environmental Awareness	3.5	0.8	2	5	3	3	3	3	0.02	0.10	0.99	Normal
Social Media Usage	2.2	0.7	1	4	2	1	3	2	0.07	0.30	0.99	Normal
Digital Literacy	3.0	0.9	1	5	3	2	4	3	0.06	0.40	0.99	Normal
Online Learning	2.5	0.8	1	4	2	1	3	2	0.08	0.50	0.98	Normal

Figure 9

1	M N E K W D T N S S E N W H P I W N V N	20
21	D T K H H L Y S D I N I T Y V N Y Y L H	40
	I	
41	Q P Q <u>V A A I F I I S Y F L I F F L C M</u>	60
61	<u>M G N T V V C F I V M R N K H M H T V T</u>	80
	II	
81	<u>N L F I L N L A I S D L L V G I F C M P</u>	100
101	<u>I T L L D N I I A G W P F G N T M C K I</u>	120
	III	
121	S G <u>L V Q G I S V A A S V F T L V A I A</u>	140
141	<u>V D R F Q C V V Y P F K P K L T I K T A</u>	160
	IV	
161	<u>F V I I M I I W V L A I T I M S P S A V</u>	180
181	M L H V Q E E K Y Y R V R L N S Q N K T	200
201	S P V Y W C R E D W P N Q E M R K I Y T	220
	V	
221	<u>T V L F A N I Y L A P L S L I V I M Y G</u>	240
241	<u>R I G I S L F R A A V P H T G R K N Q E</u>	260
261	Q W H V V S R K K Q K <u>I I K M L L I V A</u>	280
	VI	
281	<u>L L F I L S W L P L W T' L M M L S D Y A</u>	300
301	D L S P N E L Q I I N I Y I <u>Y P F A H W</u>	320
	VII	
321	<u>L A F G N S S V N P I I Y G F F N E N F</u>	340
341	R R G F Q E A F Q L Q L C Q K R A K P M	360
361	E A Y A L K A K S H V L I N T S N Q L V	380
381	Q E S T F Q N P H G E T L L Y R K S A E	400
401	K P Q Q E L V M E E L K E T T N S S E I	420

Figure 10

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rNPFF1  MEAEPSQPPNGSWPLGQNGSDVETSMAT..SLTFSSYYQHSSPVAAMFIA 48
      | . . . . | . | . : . : : . | | | | | |
hNPFF2  MNEKWDTNSSSENWHPIWNVNDTKHHLYS DINIT YVNYYLHQ PQVA AIFII 50

rNPFF1  AYVLIFLLCMVGNTLVCFIVLKNRHMRTVTNMFILNLAVSDLLVGIFCMP 98
      . | | | | | | | | | | | | | | | | | | | | | | | | | | | |
hNPFF2  SYFLIFFLCMMGNTVVC FIVMRNKHMH T VTNLFILNL AISDLLVGIFCMP 100

rNPFF1  TTLVDNLITGWPF DNATCKMSGLVQGM SVSASVFTLV AIAVERFRCIVHP 148
      | | . | | : : | | | | | | | | | | | | | | | | | | | | | |
hNPFF2  ITLLDN11AGWPF GNTMCKISGLVQGISVAASVFTLV AIAVDRFQC VVYD 150

rNPFF1  FREKLT LRKALFTI AIVIALALLIMCPSAVTLTVTREEHH.FMLDARNRS 197
      | : | | | : : | | | : | | | | | | | | | | | | | | | | | |
hNPFF2  FKPKLTIKTAFV IIMIIWVLAITIMSPSAVMLHVQEEKY YRVRLNSQNKT 200

rNPFF1  YPLYSCWEAWPEKGM RKVYTAVLFAHIYLVPLALIVVMYVRIARKLCQAP 247
      | . | | | | | . | | | : | | | | | | | | | | | | | | | | | |
hNPFF2  SPVYWCREDWPNQEMRK IYTTVLFANIYLA PLSLIVIMYGRIGISLFRAA 250

rNPFF1  GPARDTEEAVAEGGR TSRRRARV VHM LVMVALFFTL SWLPLWVLLLLIDY 297
      | . . . : | | : : : | | . | | | | | | | | | | | | | | | |
hNPFF2  VPHTGRKNQ.EQWHV VSRKKQKI IKMLLIVALLFILSWLPLWTLMMLSDY 299

rNPFF1  GELSELQLHLLSVYAFPLAHWLAFFHSSANPIIYG YFNENFRRGFQAAFR 347
      : | | : | : : : | : | | | | | | | | | | | | | | | | | | | | |
hNPFF2  ADLSPNELQIINIYIYPFAHWLA FGNSSVNPIIYGFFNENFRRGFQEA FQ 349

rNPFF1  AQLCWPPWAAHKQAYSERPNRLLRRRVVVDVQPSDGLP.SESGPSSGVP 396
      | | | . . . . | . . . | | | | | | | | | | | | | | | |
hNPFF2  LQLCQKRAKPM EAYALKAKSHVLINTSNQLVQESTFQNP HGETLLYRKSA 399

rNPFF1  GPGRPLPLRNGRVAHQDGPGE GPGCNHMLPTIPAWNI 432
      . | . . |
hNPFF2  EKPQQELVMEELKET TNSSEI..... 420

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Figure 11

1 ATGAGGGGAGCCCTCCAGCCTCCCAACAGCAGTTGGCCCCTAAGTCAGAAATGGGACT 60  
61 AACACTGAGGCCACCCCGGCTACAAACCTCACCTTCTCCTCCTACTATCAGCACACCTCC 120  
121 CCTGTGGGGCCCATGTTTATTGTGGCCCTATGCGCTCATCTTCCCTGCTCTGCATGGTGGGC 180  
181 AACACCCTGGTCTGTTTCATCGTGCTCAAGAACCGGCACATGCATACTGTCAACCAACATG 240  
241 TTCATCCTCAACCTGGCTGTCAAGTACCTGCTGGTGGGCACTTCTGCATGCCACCAACC 300  
301 CTTGTGGACAACCTCATCACTGGGTGGCCCTTCGACAATGCCACATGCAAGATGAGCGGC 360  
361 TTGGTGCAGGGCATGTCTGTGTCGGCTTCCGTTTTCACACTGGTGGCCATTGCTGTGGAA 420  
421 AGGTTCCGCTGCATCGTGCACCCCTTTCGGCGAGAAAGCTGACCCCTGCCGAAGGCGCTCGTC 480  
481 ACCATCGCCGTCACTTGGGCCCTTGGCGCTGCTCATCATGTGTCCCTCGGCCGTCAAGCTG 540  
541 ACCGTACCCGTGAGGAGCACCACTTCATGGTGGACGCCCGAACCCGCTCCTACCCCTCTC 600  
601 TACTCCTGCTGGGAGGCCTGGCCCCGAGAAGGGCATGCGCAGGGTCTACACCACCTGTGCTC 660  
661 TTCTCGCACATCTACCTGGCGCCGCTGGCGCTCATCGTGGTCACTACGCCCGCATCGCG 720  
721 CGCAAGCTCTGCCAGGCCCCGGGCCCCCGGGGGCGAGGAGGCTGCGGACCCCGGA 780  
781 GCATCGGGGCGCAGAGCGCGGTGGTGCACATGCTGGTCACTGGTGGCGCTGTTCTTCACG 840  
841 CTGTCCCTGGCTGCCGCTCTGGGCGCTGCTGCTCATCGACTACGGGCAGCTCAGCGCG 900  
901 CCGCAGCTGCACCTGGTCAACCGTCTACGCCCTTCCCTTCGCGCACTGGCTGGCCCTTCTTC 960  
961 AACAGCAGCGCCAACCCCATCATCTACGGCTACTTCAACGAGAACCTTCCGCCGCGGCTTC 1020  
1021 CAGGCCGCTTCCGGCCCCGCTCTGCCCGCCCGCTCGGGGAGCCACAAGGAGGCCCTAC 1080  
1081 TCCGAGCGGGCCCCGGGCTTCTGACAGCGGGTCTTCTGTTGGTGGTGGGCCCCAGCGAC 1140  
1141 TCCGGGCTGCCCCCTCTGAGTCGGGGCCCTAGCAGTGGGGCCCCCAGGCCCGGCCCTCCCC 1200  
1201 CTGCGGAATGGGCGGGTGGCTCACACGGCTTGCCCCAGGAAGGCCCTGGCTGCTCCCCAC 1260  
1261 CTGCCCCCTCACCATTCAGCCTGGGATATCTGA 1293

Figure 12

1 M E G E P S Q P P N S S W P L S Q N G T 20  
21 N T E A T P A T N L T F S S Y Y Q H T S 40  
41 P V A A M F I V A Y A L I F L L C M V G 60  
61 N T L V C F I V L K N R H M H T V T N M 80  
81 F I L N L A V S D L L V G I F C M P T T 100  
101 L V D N L I T G W P F D N A T C K M S G 120  
121 L V Q G M S V S A S V F T L V A I A V E 140  
141 R F R C I V H P F R E K L T L R K A L V 160  
161 T I A V I W A L A L L I M C P S A V T L 180  
181 T V T R E E H H F M V D A R N R S Y P L 200  
201 Y S C W E A W P E K G M R R V Y T T V L 220  
221 F S H I Y L A P L A L I V V M Y A R I A 240  
241 R K L C Q A P G P A P G G E E A A D P R 260  
261 A S R R R A R V V H M L V M V A L F F T 280  
281 L S W L P L W A L L L L I D Y G Q L S A 300  
301 P Q L H L V T V Y A F P F A H W L A F F 320  
321 N S S A N P I I Y G Y F N E N F R R G F 340  
341 Q A A F R A R L C P R P S G S H K E A Y 360  
361 S E R P G G L L H R R V F V V V R P S D 380  
381 S G L P S E S G P S S G A P R P G R L P 400  
401 L R N G R V A H H G L P R E G P G C S H 420  
421 L P L T I P A W D I 430

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1	M E G E P S Q P P N S S W P L S Q N G T	20
21	N T E A T P A T N L T F S S Y Y Q H T S	40
	I	
41	<u>P V A A M F I V A Y A L I F L L C M V G</u>	60
61	<u>N T L V C F I V L K N R H M H T V T N M</u>	80
	II	
81	<u>F I L N L A V S D L L V G I F C M P T T</u>	100
101	<u>L V D N L I T G W P F D N A T C K M S G</u>	120
	III	
121	<u>L V Q G M S V S A S V F T L V A I A V E</u>	140
141	R F R C I V H P F R E K L T L R K <u>A L V</u>	160
	IV	
161	<u>T I A V I W A L A L L I M C P S A V T L</u>	180
181	T V T R E E H H F M V D A R N R S Y P L	200
201	Y S C W E A W P E K G M R R V Y <u>T T V L</u>	220
	V	
221	<u>F S H I Y L A P L A L I V V M Y A R I A</u>	240
241	R K L C Q A P G P A P G G E E A A D P R	260
	VI	
261	A S R R R A R <u>V V H M L V M V A L F F T</u>	280
281	<u>L S W L P L W A L L L L I D Y G Q L S A</u>	300
301	P Q L H L V T V Y A <u>F P F A H W L A F F</u>	320
	VII	
321	<u>N S S A N P I I Y G Y F N E N F R R G F</u>	340
341	Q A A F R A R L C P R P S G S H K E A Y	360
361	S E R P G G L L H R R V F V V V R P S D	380
381	S G L P S E S G P S S G A P R P G R L P	400
401	L R N G R V A H H G L P R E G P G C S H	420
421	L P L T I P A W D I	430

Figure 14

hNPFF2 1 MNEKWDTNSSSENWHPIWNVNDTKHHLYSDINITYVNYYLHQPVAAIFII 50  
 . : . | . | | | : : . | | | | :  
 hNPFF1 1 ..MEGEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAMFIV 48  
 hNPFF2 51 SYFLIFFLCMMGNTVVC FIVMRNKHMTVTNLFILNLAISDLLVGIFCMP 100  
 . | | | | | . | | | | : : | | | | : | | | | |  
 hNPFF1 49 AYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMP 98  
 hNPFF2 101 ITLLDNIIAGWPFNGTMCKISGLVQGISVAASVFTLVAVDRFQCVVYP 150  
 | | . | : | | | | | | . | | | | | : | | . | : |  
 hNPFF1 99 TTLVDNLITGWPFDNATCKMSGVLQGMSVSASVFTLVAVRFRFCIVHP 148  
 hNPFF2 151 FKPKLTIKTAFVIIMI IWVLAITIMSPSAVMLHVQEEKYYRVRLNSQNKT 200  
 | : | | : : | | : | | | | | | | | | | : : | :  
 hNPFF1 149 FREKLTLRKALVTIAVIWALALLIMCPASVTLTVTREEHH.FMVDARNRS 197  
 hNPFF2 201 SPVYWCREDPNQEMRKIYTTVL FANIYLAPLSLIVIMYGRIGISLFRAA 250  
 . | | | | | . | | : | | | | | . | | : | | | |  
 hNPFF1 198 YPLYSCWEAWPEKGMRRVYTTVLFSHIYLA PLALIVVMYARIARKLCQAP 247  
 hNPFF2 251 VPHTGRKNQE QWHVVS RKKQKIIKMLLIVALLFILSWLPLWTLMLSDYA 300  
 | | . | : : : : | | . | | | | | | : : | |  
 hNPFF1 248 GPAPGGEEAADPR.ASRRRARVVHMLVMVALFFTLSWLPLWALLLLIDYG 296  
 hNPFF2 301 DLSPNELQIINIYIYPFAHWLAFGNSSVNPIIYGFFNENFRRGFQEAQQL 350  
 | | : | : : | : | | | | | | | | | : | | | | |  
 hNPFF1 297 QLSAPQLHLVTVYAFPF AHWLAFNSSANPIIYGYFENENFRRGFQAA FRA 346  
 hNPFF2 351 QLCQKRAKPM EAYALKAKSHVLINTSNQLVQESTFQNP HGETLLYRKSAE 400  
 . | | | | : | : . . | . . | . .  
 hNPFF1 347 RLC.PRPSGSHKEAYSERPGGLLHRRVFVVVRPSD SGLPSESGPSSGAPR 395  
 hNPFF2 401 KPQQELVMEELKETTNSSEI\*..... 420  
 . | . |  
 hNPFF1 396 PGR LPLRNGRV AHHGLPREGPGCSHLPLTIPAWDI\* 431

Figure 15A

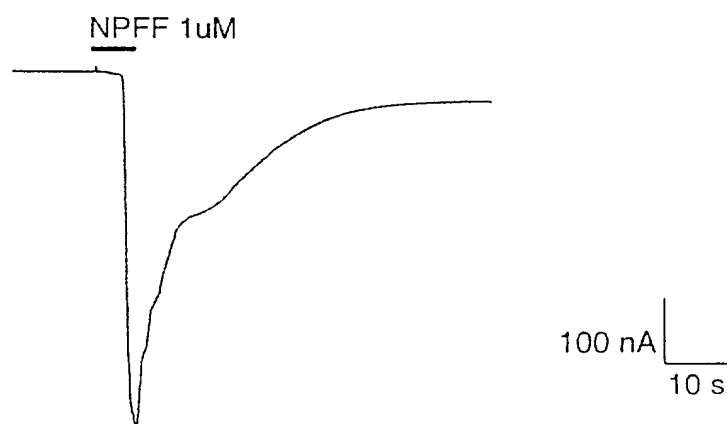


Figure 15B

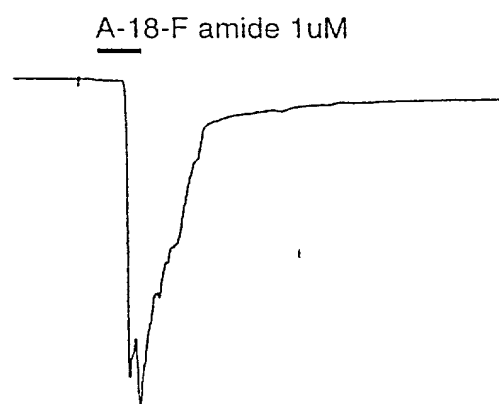


Figure 15C

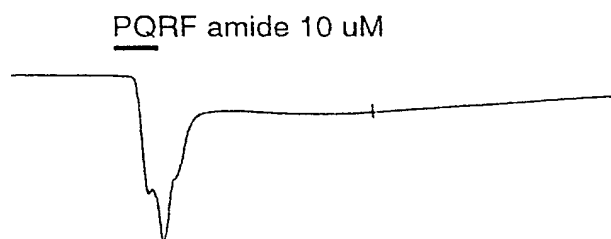


Figure 16A

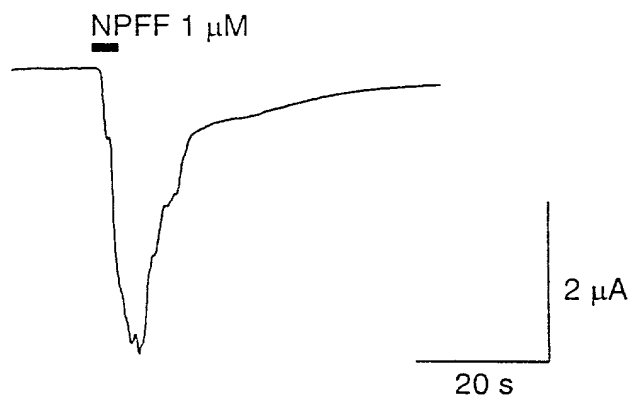


Figure 16B

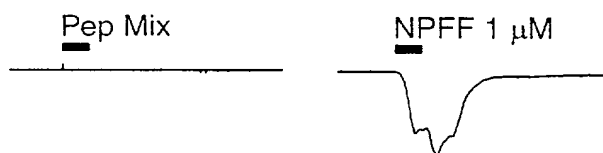


Figure 16C

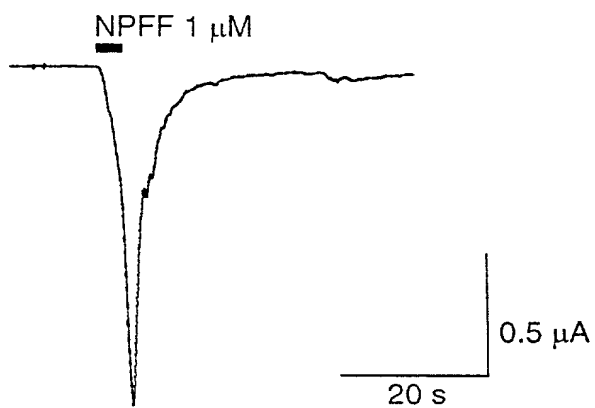




Figure 17A

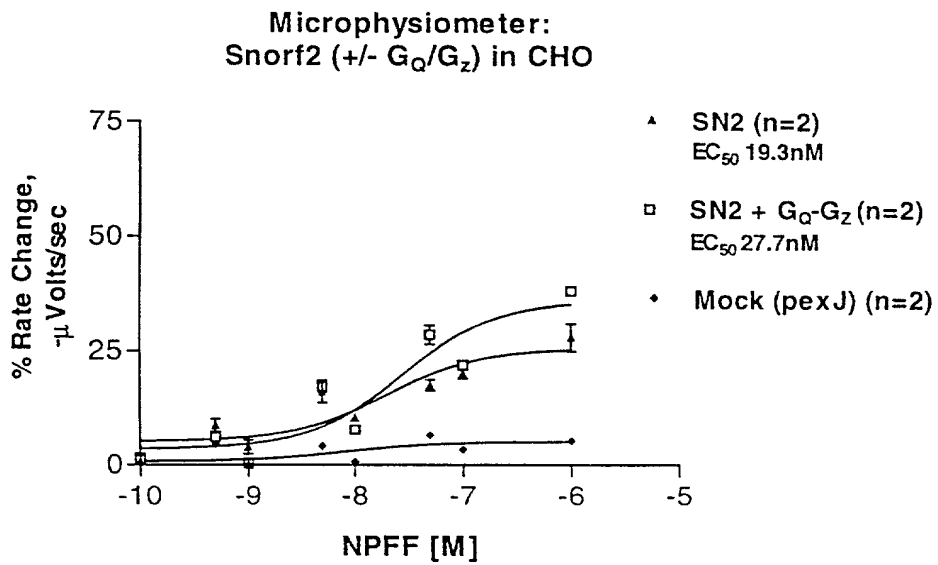


Figure 17B

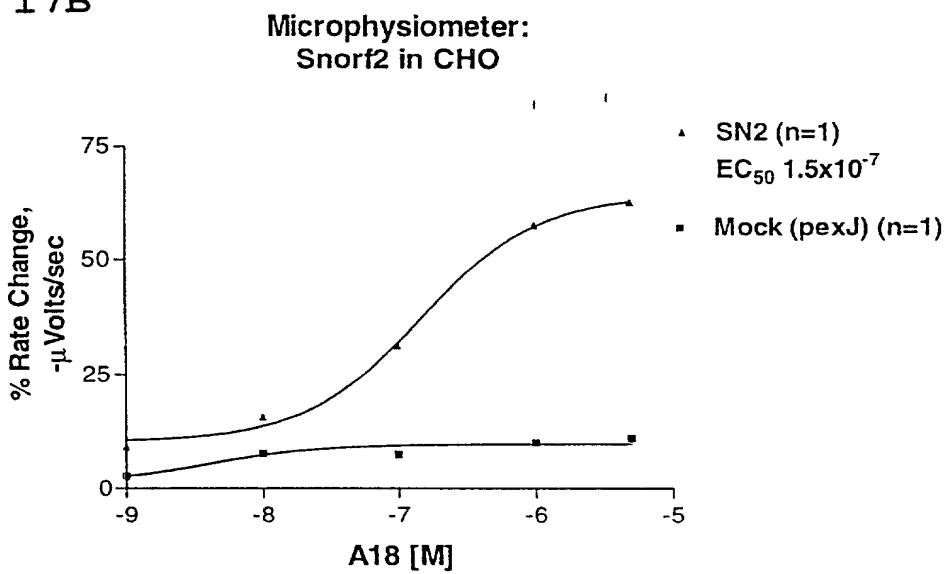


Figure 18A

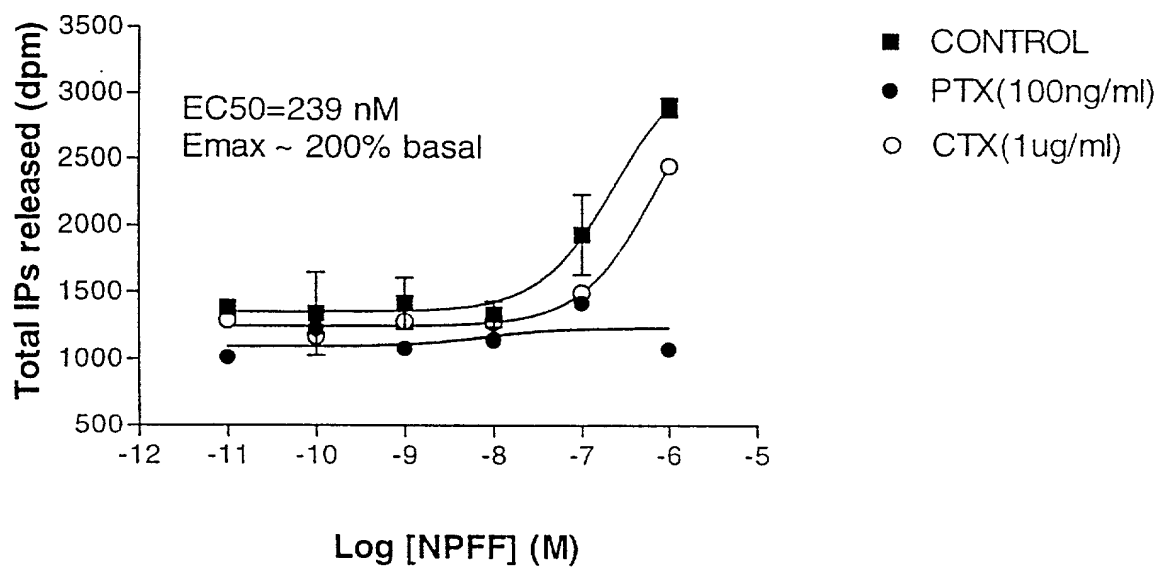


Figure 18B

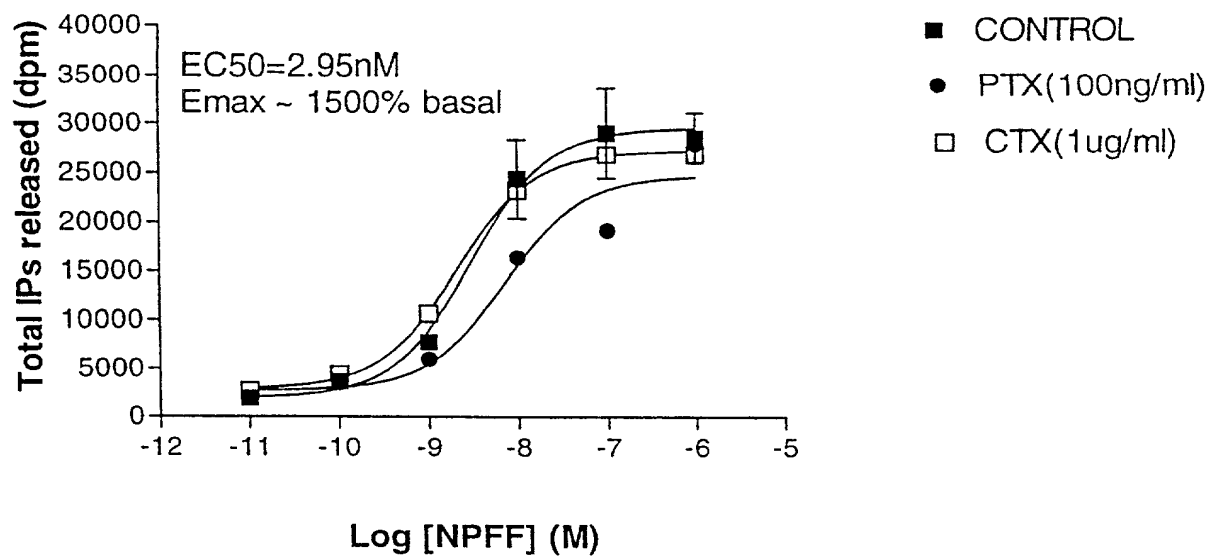


Figure 19

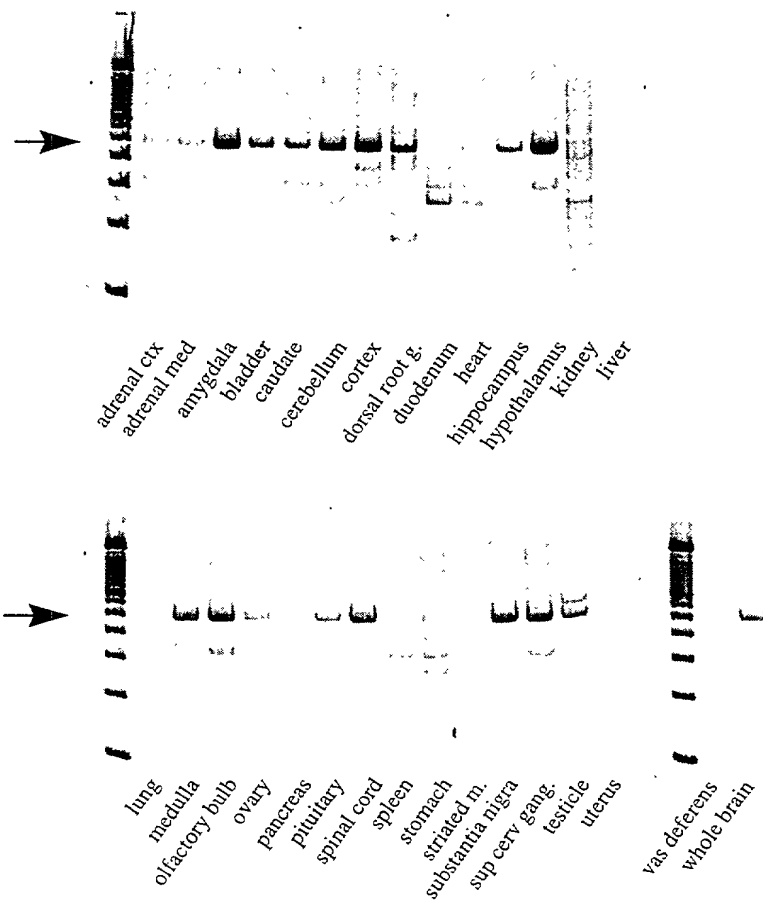


Figure 20

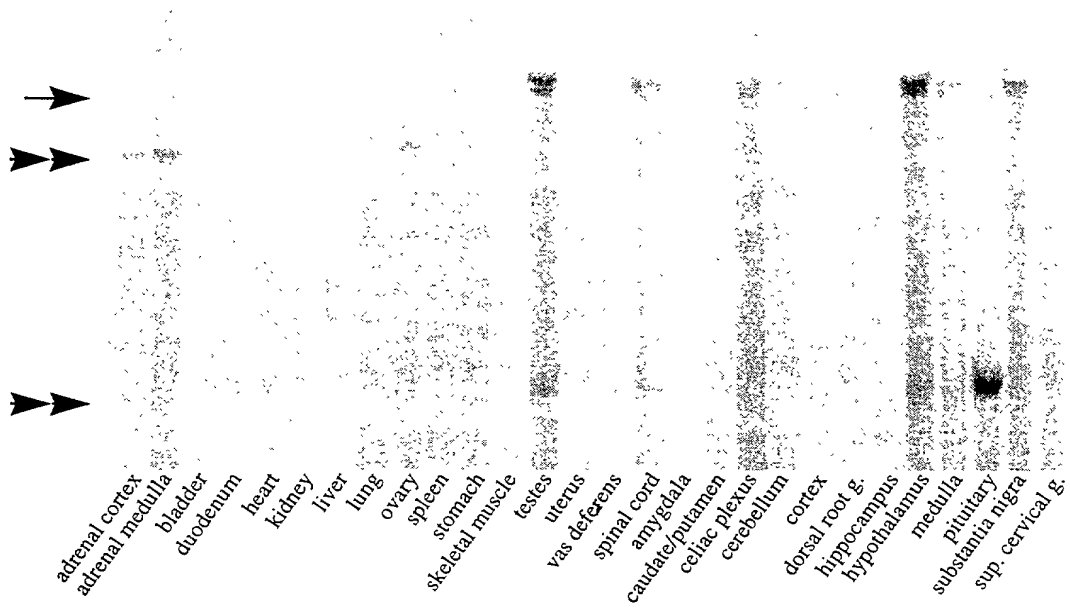


Figure 21

